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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Tue Jun 05 18:58:10 EDT 2007

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Reviewer Comments:

<210> 3
<211> 16
<212> PRT
<213> Artificial Sequence
<220>
<223> synthetic bromodomain peptide
<220>
<221> Xaa
<222> (2)..(4)
<223> Xaa is a maximum of three amino acids. Each of these can be any amino acid. One may be missing.

The above <222> response denotes Xaa's at locations 2 through 4; however, "Pro" is at location 3. Same type of error throughout sequence 3 and sequence 43.

<210> 7
<211> 110
<212> PRT
<213> Homo sapiens, bromodomain peptide

The <213> response above is erroneous; the response should only show "Homo sapiens." Please move "bromodomain peptide" to the <220>-<223> section.

<210> 34
<211> 112
<212> PRT

<213> Description of unknown organism, see Jeanmougin et al.,
Trends in Biochem. Sci. 22:151-153 (1997)

Per 1.823 of Sequence Rules, the only valid <213> response is "Unknown"; do not include any other explanation on the <213> line. The "see Jeanmougin..." is not a valid explanation of "Unknown." Please give the source of the genetic material in the <220>-<223> section. Same error in sequence 35.

Input Set:

Output Set:

Started: 2007-06-05 17:13:10.137

Finished: 2007-06-05 17:13:14.253

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 116 ms

Total Warnings: 6

Total Errors: 19

No. of SeqIDs Defined: 44

Actual SeqID Count: 44

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)



SEQUENCE LISTING

<1> Zhou, Ming-Ming
Aggarwal, Aneel

<120> Methods of Identifying Modulators of Bromodomains

<130> 2459-1-003

<140> 09510314

<141> 2007-06-05

<150> 09/510,314

<151> 2000-02-22

<160> 44

<170> PatentIn version 3.0

<210> 1

<211> 3014

<212> DNA

<213> Homo sapiens

<400> 1

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<211> 832
<212> PRT
<213> Homo sapiens

<400> 2

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Pro Pro Ala Pro Pro Gln Gly Ser Pro Cys Ala Ala Ala Ala Gly Gly
35 40 45

Ser Gly Ala Cys Gly Pro Ala Thr Ala Val Ala Ala Ala Gly Thr Ala
50 55 60

Glu Gly Pro Gly Gly Gly Gly Ser Ala Arg Ile Ala Val Lys Lys Ala
65 70 75 80

Gln Leu Arg Ser Ala Pro Arg Ala Lys Lys Leu Glu Lys Leu Gly Val
85 90 95

Tyr Ser Ala Cys Lys Ala Glu Glu Ser Cys Lys Cys Asn Gly Trp Lys
100 105 110

Asn Pro Asn Pro Ser Pro Thr Pro Pro Arg Ala Asp Leu Gln Gln Ile
115 120 125

Ile Val Ser Leu Thr Glu Ser Cys Arg Ser Cys Ser His Ala Leu Ala
130 135 140

Ala His Val Ser His Leu Glu Asn Val Ser Glu Glu Glu Met Asn Arg
145 150 155 160

Leu Leu Gly Ile Val Leu Asp Val Glu Tyr Leu Phe Thr Cys Val His
 165 170 175

Lys Glu Glu Asp Ala Asp Thr Lys Gln Val Tyr Phe Tyr Leu Phe Lys
 180 185 190

Leu Leu Arg Lys Ser Ile Leu Gln Arg Gly Lys Pro Val Val Glu Gly
 195 200 205

Ser Leu Glu Lys Lys Pro Pro Phe Glu Lys Pro Ser Ile Glu Gln Gly
 210 215 220

Val Asn Asn Phe Val Gln Tyr Lys Phe Ser His Leu Pro Ala Lys Glu
 225 230 235 240

Arg Gln Thr Ile Val Glu Leu Ala Lys Met Phe Leu Asn Arg Ile Asn
 245 250 255

Tyr Trp His Leu Glu Ala Pro Ser Gln Arg Arg Leu Arg Ser Pro Asn
 260 265 270

Asp Asp Ile Ser Gly Tyr Lys Glu Asn Tyr Thr Arg Trp Leu Cys Tyr
 275 280 285

Cys Asn Val Pro Gln Phe Cys Asp Ser Leu Pro Arg Tyr Glu Thr Thr
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Gln Val Phe Gly Arg Thr Leu Leu Arg Ser Val Phe Thr Val Met Arg
 305 310 315 320

Arg Gln Leu Leu Glu Gln Ala Arg Gln Glu Lys Asp Lys Leu Pro Leu
 325 330 335

Glu Lys Arg Thr Leu Ile Leu Thr His Phe Pro Lys Phe Leu Ser Met
 340 345 350

Leu Glu Glu Glu Val Tyr Ser Gln Asn Ser Pro Ile Trp Asp Gln Asp
 355 360 365

Phe Leu Ser Ala Ser Ser Arg Thr Ser Gln Leu Gly Ile Gln Thr Val
 370 375 380

Ile Asn Pro Pro Pro Val Ala Gly Thr Ile Ser Tyr Asn Ser Thr Ser
 385 390 395 400

Ser Ser Leu Glu Gln Pro Asn Ala Gly Ser Ser Ser Pro Ala Cys Lys
 405 410 415

Ala Ser Ser Gly Leu Glu Ala Asn Pro Gly Glu Lys Arg Lys Met Thr
 420 425 430

Asp Ser His Val Leu Glu Glu Ala Lys Lys Pro Arg Val Met Gly Asp
 435 440 445

Ile Pro Met Glu Leu Ile Asn Glu Val Met Ser Thr Ile Thr Asp Pro
 450 455 460

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Arg Asp Glu Ala Ala Arg Leu Glu Glu Arg Arg Gly Val Ile Glu Phe			
	485	490	495
His Val Val Gly Asn Ser Leu Asn Gln Lys Pro Asn Lys Lys Ile Leu			
	500	505	510
Met Trp Leu Val Gly Leu Gln Asn Val Phe Ser His Gln Leu Pro Arg			
	515	520	525
Met Pro Lys Glu Tyr Ile Thr Arg Leu Val Phe Asp Pro Lys His Lys			
	530	535	540
Thr Leu Ala Leu Ile Lys Asp Gly Arg Val Ile Gly Gly Ile Cys Phe			
545	550	555	560
Arg Met Phe Pro Ser Gln Gly Phe Thr Glu Ile Val Phe Cys Ala Val			
	565	570	575
Thr Ser Asn Glu Gln Val Lys Gly Tyr Gly Thr His Leu Met Asn His			
	580	585	590
Leu Lys Glu Tyr His Ile Lys His Asp Ile Leu Asn Phe Leu Thr Tyr			
	595	600	605
Ala Asp Glu Tyr Ala Ile Gly Tyr Phe Lys Lys Gln Gly Phe Ser Lys			
	610	615	620
Glu Ile Lys Ile Pro Lys Thr Lys Tyr Val Gly Tyr Ile Lys Asp Tyr			
625	630	635	640
Glu Gly Ala Thr Leu Met Gly Cys Glu Leu Asn Pro Arg Ile Pro Tyr			
	645	650	655
Thr Glu Phe Ser Val Ile Ile Lys Lys Gln Lys Glu Ile Ile Lys Lys			
	660	665	670
Leu Ile Glu Arg Lys Gln Ala Gln Ile Arg Lys Val Tyr Pro Gly Leu			
	675	680	685
Ser Cys Phe Lys Asp Gly Val Arg Gln Ile Pro Ile Glu Ser Ile Pro			
	690	695	700
Gly Ile Arg Glu Thr Gly Trp Lys Pro Ser Gly Lys Glu Lys Ser Lys			
705	710	715	720
Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser Ile Leu			
	725	730	735
Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu Pro Val			
	740	745	750
Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Phe Pro Met			
	755	760	765

Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr Val Ser
770 775 780

Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn Cys Lys
785 790 795 800

Glu Tyr Asn Ala Ala Glu Ser Glu Tyr Tyr Lys Cys Ala Asn Ile Leu
805 810 815

Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly Leu Ile Asp Lys
820 825 830

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic bromodomain peptide

<220>

<221> Xaa

<222> (2)..(4)

<223> Xaa is a maximum of three amino acids. Each of these can be
any amino acid. One may be missing.

<220>

<221> Xaa

<222> (4)..(11)

<223> Xaa is a maximum of eight amino acids. Each of these can be
any amino acid. One, two, or three may be missing.

<220>

<221> Xaa

<222> (5)..(5)

<223> Xaa is a single amino acid that is either Pro, Lys, or His.

<220>

<221> Xaa

<222> (6)..(6)

<223> Xaa is any single amino acid.

<220>

<221> Xaa

<222> (8)..(8)

<223> Xaa is a single amino acid that can be either Tyr, Phe, or His.

<220>

<221> Xaa

<222> (9)..(13)

<223> Xaa is any amino acid.

<220>
<221> Xaa
<222> (15)..(15)
<223> Xaa is a single amino acid that can be either Met, Ile, or Val.

<400> 3

Phe Xaa Pro Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asp
1 5 10 15

<210> 4
<211> 12
<212> PRT
<213> Artificial Sequence
<220>
<223> synthetic bromodomain peptide

<220>
<221> Xaa
<222> (6)..(6)
<223> Xaa represents an acetyl-lysine

<400> 4

Ile Ser Tyr Gly Arg Xaa Lys Arg Arg Gln Arg Arg
1 5 10

<210> 5
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic bromodomain peptide

<220>
<221> Xaa
<222> (8)..(8)
<223> Xaa represents an acetyl lysine.

<400> 5

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1 5 10

<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic bromodomain peptide

<220>

<221> Xaa

<222> (8)..(8)

<223> Xaa represents an acetyl lysine.

<400> 6

Gln Ser Thr Ser Arg His Lys Xaa Leu Met Phe Lys Thr Glu
1 5 10

<210> 7

<211> 110

<212> PRT

<213> Homo sapiens, bromodomain peptide

<400> 7

Ser Lys Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser
1 5 10 15

Ile Leu Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu
20 25 30

Pro Val Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Ser
35 40 45

Pro Met Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr
50 55 60

Val Ser Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn
65 70 75 80

Cys Lys Glu Tyr Asn Ala Pro Glu Ser Glu Tyr Tyr Lys Cys Ala Asn
85 90 95

Ile Leu Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly
100 105 110

<210> 8

<211> 110

<212> PRT

<213> Homo sapiens

<400> 8

Gly Lys Glu Leu Lys Asp Pro Asp Gln Leu Tyr Thr Thr Leu Lys Asn
1 5 10 15

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20 25 30

Pro Val Lys Lys Ser Glu Ala Pro Asp Tyr Tyr Glu Val Ile Arg Phe

35

40

45

Pro Ile Asp Leu Lys Thr Met Thr Glu Arg Leu Arg Ser Arg Tyr Tyr
50 55 60

Val Thr Arg Lys Leu Phe Val Ala Asp Leu Gln Arg Val Ile Ala Asn
65 70 75 80

Cys Arg Glu Tyr Asn Pro Pro Asp Ser Glu Tyr Cys Arg Cys Ala Ser
85 90 95

Ala Leu Glu Lys Phe Phe Tyr Phe Lys Leu Lys Glu Gly Gly
100 105 110

<210> 9

<211> 109

<212> PRT

<213> *Tetrahymena thermophila*

<400> 9

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20 25 30

Val Asn Lys Asp Asp Val Pro Asp Tyr Tyr Asp Val Ile Thr Asp Pro
35 40 45

Ile Asp Ile Lys Ala Ile Glu Lys Lys Leu Gln Asn Asn Gln Tyr Val
50 55 60

Asp Lys Asp Gln Phe Ile Lys Asp Val Lys Arg Ile Phe Thr Asn Ala
65 70 75 80

Lys Ile Tyr Asn Gln Pro Asp Thr Ile Tyr Tyr Lys Ala Ala Lys Glu
85 90 95

Leu Glu Asp Phe Val Glu Pro Tyr Leu Thr Lys Leu Lys
100 105

<210> 10

<211> 109

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

Ala Gln Arg Pro Lys Arg Gly Pro His Asp Ala Ala Ile Gln Asn Ile
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20 25 30

Val Asn Lys Glu Glu Val Pro Asp Tyr Tyr Asp Phe Ile Lys Glu Pro
35 40 45

Met Asp Leu Ser Thr Met Glu Ile Lys Leu Glu Ser Asn Lys Tyr Gln
50 55 60

Lys Met Glu Asp Phe Ile Tyr Asp Ala Arg Leu Val Phe Asn Asn Cys
65 70 75 80

Arg Met Tyr Asn Gly Glu Asn Thr Ser Tyr Tyr Lys Tyr Ala Asn Arg
85 90 95

Leu Glu Lys Phe Phe Asn Asn Lys Val Lys Glu Ile Pro
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<210> 11

<211> 112

<212> PRT

<213> Homo sapiens

<400> 11

Lys Lys Ile Phe Lys Pro Glu Glu Leu Arg Gln Ala Leu Met Pro Thr
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Leu Glu Ala Leu Tyr Arg Gln Asp Pro Glu Ser Leu Pro Phe Arg Gln
20 25 30

Pro Val Asp Pro Gln Leu Leu Gly Ile Pro Asp Tyr Phe Asp Ile Val
35